

Amendments to the Claims:

1-25. (Withdrawn)

26. (Currently Amended) A ~~method~~ computer system for evaluating user-supplied genomics data, the system comprising:

a computer comprising using a structured database to store and access genomics information, wherein the computer permits the computation of complex relationships among genes and/or gene products found within the genomics information

that permits the computation of complex relationships among genes and/or gene products contained in the database, comprising:

wherein the computer is configured to:

- (a) ~~defining~~ define a profile model based on one or more profile definition criterion;
- (b) ~~building~~ build a collection of profiles according to the profile model using genomics information stored in the database;
- (c) ~~identifying~~ identify one or more profiles that overlap at least a portion of ~~[[the]]~~ a user-supplied genomics data and ~~determining~~ determine, for each such overlapped profile, whether the overlap is statistically significant; and
- (d) ~~analyzing~~ analyze one or more statistically significant profiles together with the user supplied genomics data including ~~inspecting~~ inspection of database-asserted biological interactions embodied in the one or more statistically significant profiles.

27. (Currently Amended) The ~~method~~ computer system of claim 26, wherein the computer is further configured to including the step of pre-generating pre-generate a profile library containing a profile for each one of a genomic information type in the database according to the profile model.

28. (Currently Amended) The ~~method~~ computer system of claim 27, wherein the profiles are pre-generated from a graph structure.

29. (Currently Amended) The ~~method~~ computer system of claim 26, ~~wherein the computer is further configured to comprising the step of generating~~ generate profiles by querying the database for information matching the one or more profile definition criterion.

30. (Currently Amended) The ~~method~~ computer system of claim 28, wherein the ~~determining determination of statistical significance step~~ includes the ~~step of computing~~ computation of a probability of overlap as a function of information contained in the database.

31. (Currently Amended) The ~~method~~ computer system of claim 26, wherein the genomic information type is one of a gene, gene product and biological process.

32. (Currently Amended) The ~~method~~ computer system of claim 26, wherein the user-supplied genomics data is differential gene expression data ~~and the analyzing step further includes one of the steps of:~~

(1) ~~—identifying a new use for a known therapy wherein the gene expression data relates to a pathway affected by the known therapy;~~

(2) ~~—prioritizing candidate development compounds for further development wherein the gene expression data relates to the target of one or more candidate development compounds and the analyzing step includes giving higher priority to development compounds on the basis of whether or not they are likely to result in an undesirable effect based on their involvement in other biological pathways as embodied in the profile; and~~

(3) ~~—identifying disease-related pathways wherein the disease is a side effect of drug therapy, wherein the gene expression data relates to the target affected by the drug therapy and the alternative pathways that are also affected by the drug or the drug discovery target and that result in an undesirable phenotype are embodied in the profile.~~

33. (Currently Amended) The ~~method~~ computer system of claim [[26]] 32, wherein the genomics data is differential gene expression data ~~relating~~ relates to a particular disease; ~~and wherein the analyzing step further includes the step of validating whether the gene expression data are~~ genotypic

~~markers for the disease state according to whether a database asserted biological association related to the disease state, which is shared among a plurality of overlapped profiles, is statistically significant.~~

34. (Currently Amended) The ~~method~~ computer system of claim 26, wherein the profile generation criterion include one or more of a biological process, number of genes, organismal, gene connectivity, edge connectivity, findings source type, experiment context, and tissue consistency criterion.

35. (Currently Amended) The ~~method~~ computer system of claim 26, wherein the profiles are generated from a seed node and the ~~inspecting~~ inspection of database-asserted biological interactions ~~step~~ focuses on the biological interactions emanating from the seed node.

36. (Currently Amended) The ~~method~~ computer system of claim 35, wherein the seed is one of a gene, gene product and biological process genomic data type.

37. (Currently Amended) The ~~method~~ computer system of claim 26, ~~wherein the computer is further configured to comprising computing compute~~ a statistical significance for a biological association in the one or more statistically significant profiles.

38. (Currently Amended) The ~~method~~ computer system of claim [[26]] 27, wherein the ~~generating pregeneration of~~ a profile library ~~step~~ includes, for each profile generated, the ~~step of selecting selection of~~ a node for a profile based on the number of similar findings in the database that link the node to a neighboring node.

39. (Currently Amended) The ~~method~~ computer system of claim 26, ~~wherein the computer is further configured to comprising the step of displaying display~~ information related to the one or more statistically significant profiles and genomics data using a GUI.

40. (Currently Amended) The ~~method~~ computer system of claim 26, ~~wherein the computer is further configured to including the step of annotating annotate~~ the profiles with biological

associations asserted by the database including wherein the associations comprise one or more of a cellular process, molecular process, organismal process and disease process.

41. (Currently Amended) The ~~method~~ computer system of claim 40, wherein the computer is further configured to including the step of displaying display biological associations using one of a GUI and a report.

42. (Currently Amended) The ~~method~~ computer system of claim 40, wherein the annotation of profiles includes the use of using classification information found in an ontology.

43. (Currently Amended) The ~~method~~ computer system of claim 26, wherein the ~~determining determination~~ of statistical significance test includes the test of testing a null hypothesis over a discrete probability distribution, the distribution being a function of the database size, profile sizes, the user-supplied genomics data size and expression values.

44. (Currently Amended) The ~~method~~ computer system of claim [[26]] 27, wherein the ~~generating pregeneration~~ step includes generating a plurality of profile libraries[[.]] and wherein each of which corresponding profile library corresponds to a different ~~one of a plurality of~~ profile generation criterion[[s]].

45-53. (Withdrawn)

54. (New) The computer system of claim 33, wherein the computer is further configured to analyze user-supplied genomics data to identify a new use for a known therapy wherein the gene expression data relates to a pathway affected by the known therapy.

55. (New) The computer system of claim 33, wherein the computer is further configured to analyze user-supplied genomics data to prioritize candidate development compounds for further development by giving higher priority to development compounds on the basis of whether or not they are likely to result in an undesirable effect based on their involvement in other biological pathways as embodied in the profile.

56. (New) The computer system of claim 33, wherein the computer is further configured to analyze user-supplied genomics data to identify disease-related pathways wherein the disease is a side effect of drug therapy.

57. (New) The computer system of claim 33, wherein the differential gene expression data relates to a particular disease, and wherein the analyzing step further includes the step of validating whether the gene expression data are genotypic markers for the disease state according to whether a database-asserted biological association related to the disease state, which is shared among a plurality of overlapped profiles, is statistically significant.